



STIC Search Report

Biotech-Chem Library

File Copy
09/747,385
updated

STIC Database Tracking Number: 141924

TO: David Lamberston
Location: rem/2b79/2c70
Art Unit: 1636
Thursday, January 06, 2005

Case Serial Number: 09/747385

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

O'Bryen, Barbara

From: Lambertson, David
Sent: Wednesday, January 05, 2005 9:15 AM
To: O'Bryen, Barbara; Fredman, Jeffrey
Subject: RE: problem re: us09747385

Yes, I apologize for not indicating that...please cancel the oligomer search portion. In retrospect, it appears I should not have included it in the first place.

Dave.

-----Original Message-----

From: O'Bryen, Barbara
Sent: Wednesday, January 05, 2005 9:14 AM
To: Fredman, Jeffrey
Cc: Lambertson, David
Subject: FW: problem re: us09747385

Jeff,
I'll let you know the new processing times when I set up the search. What you've recommended will definitely reduce the processing time. I have one question - has the oligmer portion of the search request been cancelled, or should I also do an oligomer search on the selected fragments.

Thanks,
Barb

-----Original Message-----

From: Lambertson, David
Sent: Wednesday, January 05, 2005 8:42 AM
To: O'Bryen, Barbara
Subject: FW: problem re: us09747385

Barb,

Here is what Jeff recommended as far as improving the search. Let me know if there is anything else you need from me.

THanks a bunch,
Dave.

-----Original Message-----

From: Fredman, Jeffrey
Sent: Wednesday, January 05, 2005 7:58 AM
To: Lambertson, David
Subject: RE: problem re: us09747385

David,

I looked at the case and it is clear that for SEQ ID NOs: 6 and 15, you really only need to search a small part to see if they are out there. Since the claims are comprising and no fragments are claimed, a perfect match is essentially required. So a search of each end of the DNAs would tell you if there are any perfect hits. If there are any, it is very easy for stic to align one or two hits with the sequence at issue.

So I would recommend search nucleotides 1-250 and 9700-9955 of SEQ ID NO: 15 only. For SEQ ID NO: 6, search nucleotides 1-250 and nucleotides 5600-5887 or so. This search will run somewhat faster (If Barb could let me know how much, I would really appreciate it).

Jeff Fredman

-----Original Message-----

From: Lambertson, David
Sent: Wednesday, January 05, 2005 6:57 AM
To: Fredman, Jeffrey

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 2591.45 Seconds
(without alignments)
4049.721 Million cell updates/sec

Title: US-09-747-385-6_COPY_5600_5887

Perfect score: 288

Sequence: 1 agtcaatcaaaaaataataa.....atcatctaaattctttaatt 288

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_hcc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	92.6	32.2	1119	AG376945	Mus musculus
2	91.8	31.9	889	CNS006W4	Drosophila
3	91.4	31.7	951	AZ676519	ENTGV51TF
4	89	30.9	889	CNS006W4	Drosophila
5	88.4	30.7	417	CNS02AH7	Drosophila
6	88.4	30.7	1221	AG360812	Tetraodon
7	88.2	30.6	951	AZ676519	Mus musculus
8	87.4	30.3	613	AQ922590	RPCT-23-2
9	86.8	30.1	1119	AG376945	Mus musculus
10	86.4	30.0	613	AQ922590	RPCT-23-2
11	85.8	29.8	417	CNS02AH7	Tetraodon
12	85.6	29.7	939	BH163549	ENTRS08TR
13	85.2	29.6	433	CNS04FGC	Tetraodon
14	85.2	29.6	1101	CNS00LT2	Drosophila
15	84.6	29.4	1295	CG757539	P052-4-E0
16	84.2	29.2	1263	AG396942	Mus musculus
17	84	29.2	868	AZ676519	ENTGV51TF
18	83.8	29.1	875	CU142825	ISB1-120N
19	83.2	28.9	875	CU142825	ISB1-120N
20	83.2	28.9	1275	CU142825	ISB1-120N
21	82.8	28.7	706	CF872119	tric029xp
22	82.6	28.7	939	BH163549	ENTRS08TR
23	82.6	28.7	997	CD049644	AGENCOURT
24	82.4	28.6	433	CNS04FGC	Tetraodon

C 25	82.4	28.6	868	8	AZ673655	ENTKUI7TR
C 26	82	28.5	777	9	CNS025WB	Tetraodon
C 27	82	28.5	1152	9	CU499024	SAIU_662
C 28	81.8	28.4	1191	9	AG360928	Mus musculus
C 29	81.8	28.4	1616	3	CR734259	Tetraodon
C 30	81.4	28.3	1101	3	CNS0021J	Drosophila
C 31	81.4	28.3	1190	6	CNS02ON7	Tetraodon
C 32	80.8	28.1	1014	6	CD048535	AGENCOURT
C 33	80.6	28.0	1201	9	CNS0167M	Drosophila
C 34	80.2	27.8	483	9	CNS0119C	AGENCOURT
C 35	80.2	27.8	741	7	CR842216	Drosophila
C 36	79.8	27.7	908	8	BH156237	Drosophila
C 37	79.8	27.7	1225	9	CNS0161D	ENTRV74TF
C 38	79.6	27.6	1221	9	AG360812	Drosophila
C 39	79.4	27.6	866	9	CNS006MS	Mus musculus
C 40	79.4	27.6	1067	6	CD386564	AGENCOURT
C 41	79.2	27.5	706	7	CF872119	tric029xp
C 42	78.8	27.4	437	9	CNS03OF0	Tetraodon
C 43	78.8	27.4	866	6	CF289423	AGENCOURT
C 44	78.8	27.4	922	8	AZ548363	ENTDZ07TF
C 45	78.4	27.2	641	1	AV735039	AV735039

ALIGNMENTS

RESULT 1
AG376945
LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AG376945 1119 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-184M01.T7, genomic survey
sequence.
AG376945 GI:47988150
GSS.
Mus musculus molossinus
Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 1119)
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukuba, Ibaraki, 305-0856, Japan
(E-mail:hattori@sc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@tc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@tc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACE3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. 1119
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-184M01.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 12:44:02 ; Search time 1314.48 Seconds
(without alignments)
1237.519 Million cell updates/sec

Title: US-09-747-385-6_COPY_5600_5887
Perfect score: 288
Sequence: 1 agtcaatcaaaaaataaa.....atcatctaaatctttaaaat 288

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	76.2	26.5	3673778	15	US-10-312-841-2
C 2	75.8	26.3	10039	15	Sequence 2, Appli
C 3	72.6	25.2	585	18	Sequence 2015, Ap
C 4	69.8	24.2	5908	14	Sequence 58104, A
C 5	69.8	24.2	5908	15	Sequence 93, Appl
C 6	69.8	24.2	5908	15	Sequence 105, App
C 7	69.6	24.2	6486	17	Sequence 175, App
C 8	68.6	23.8	529	18	Sequence 80, Appl
C 9	68.6	23.8	543	17	Sequence 171364, A
C 10	68.2	23.7	433	17	Sequence 10-021-323-14156
C 11	67.8	23.5	474	18	Sequence 4250, Ap
C 12	67.8	23.5	545	16	Sequence 2807, Ap
					Sequence 142212,

13	67.6	23.5	584	18	US-10-425-115-33678
14	67.2	23.3	8946	15	Sequence 33678, A
15	67.2	23.3	3673778	15	Sequence 883, App
16	67	23.3	438	16	Sequence 1, Appli
17	66.8	23.2	317	9	Sequence 79137, A
18	66.6	23.1	510	18	Sequence 2699, Ap
19	66.4	23.1	461	10	Sequence 58133, A
20	66.2	23.0	423	10	Sequence 17724, A
21	66	22.9	6436	15	Sequence 7147, Ap
22	65.8	22.8	403	18	Sequence 654, App
23	65.8	22.8	1543	16	Sequence 155989,
24	65.4	22.7	317	18	Sequence 165, App
25	65.4	22.7	603	18	Sequence 58200, A
26	65.4	22.7	12138	15	Sequence 58664, A
27	65.4	22.7	12138	16	Sequence 1601, Ap
28	64.6	22.4	368	17	Sequence 115, App
29	64.6	22.4	545	17	Sequence 5024, Ap
30	64.4	22.4	390	16	Sequence 6889, Ap
31	64.4	22.4	565	18	Sequence 72814, A
32	64.4	22.4	6171	15	Sequence 48405, A
33	64.2	22.3	1403	17	Sequence 762, App
34	64.2	22.3	8056	18	Sequence 19360, A
35	64	22.2	5753	17	Sequence 240, App
36	63.8	22.2	530	18	Sequence 146, App
37	63.8	22.2	799	16	Sequence 88475, A
38	63.6	22.1	1243	18	Sequence 88818, A
39	63.2	21.9	452	17	Sequence 13710,
40	63.2	21.9	564	17	Sequence 4768, Ap
41	63.2	21.9	1245	18	Sequence 7972, Ap
42	63.2	21.9	6112	15	Sequence 15266, A
43	63.2	21.9	21537	15	Sequence 636, App
44	63.2	21.9	3673778	15	Sequence 1972, Ap
45	63	21.9	457	17	Sequence 2, Appli
					Sequence 70141, A

ALIGNMENTS

RESULT 1
US-10-312-841-2/c
; Sequence 2, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MH
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312.841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2

Query Match	26.5%	Score	76.2	DB	15	Length	3673778
Best Local Similarity	54.9%	Pred. No.	0.065				
Matches	150	Conservative	0	Mismatches	123	Indels	0
Gaps	0						
Oy	5	AATCAAAAAATATAATATAATTAATCTACTAAGAGAGTTTAATGAAAAAGAGAGC	64				
Db	971677	AA	971678				
Oy	65	TTACGATTAGAGAAATATAAAAGATGCGAGAGACTAAATATAATTAATAAAG	124				
Db	971617	AA	971618				
Oy	125	AGGTATAGTATAATACCTCTTCTTTTAAAGTGGCTTAAATTTGATTGAGACTTCA	184				

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 64.5517 Seconds
(without alignments)
3171.212 Million cell updates/sec

Title: US-09-747-385-6_COPY_5600_5887

Perfect score: 288

Sequence: 1 agtcaatcaaaaaataaa.....atcatctaaatttttaatt 288

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71.2	24.7	196	US-09-442-054A-42	Sequence 42, Appl
2	71.2	24.7	196	US-09-442-054A-42	Sequence 42, Appl
3	59.6	20.7	731	US-08-451-405A-2	Sequence 2, Appl
4	58.8	20.4	5852	US-07-867-106-2	Sequence 2, Appl
5	58.4	20.3	2621	US-08-553-619B-8	Sequence 8, Appl
6	56.4	19.6	8607	US-10-204-708-72	Sequence 72, Appl
7	56.4	19.6	1684976	US-08-916-421B-1	Sequence 1, Appl
8	56.4	19.6	1684976	US-09-692-570-1	Sequence 1, Appl
9	56.2	19.5	1577	US-09-270-767-3138	Sequence 3138, Ap
10	56.2	19.5	1577	US-09-270-767-3138	Sequence 3138, Ap
11	55.8	19.4	20674	US-09-641-638-651	Sequence 651, App
12	55.8	19.4	20674	US-10-170-097-651	Sequence 651, App
13	55.5	19.1	6243	US-09-056-075-1	Sequence 1, Appl
14	54.6	19.0	3138	US-07-867-106-4	Sequence 4, Appl
15	54	18.8	3440	US-08-471-791-27	Sequence 27, Appl
16	54	18.8	3440	PCT-US91-01746-27	Sequence 27, Appl
17	53.6	18.6	8607	US-10-204-708-71	Sequence 71, Appl
18	52.8	18.3	5455	US-10-204-708-34	Sequence 34, Appl
19	52.6	18.3	731	US-08-451-405A-2	Sequence 2, Appl
20	52.6	18.3	2146	US-10-003-392-3	Sequence 3, Appl
21	52.6	18.3	3275	US-09-370-838-151	Sequence 151, App
22	52.6	18.3	3275	US-09-854-133-151	Sequence 151, App
23	52.4	18.2	5152	US-10-204-708-47	Sequence 47, Appl
24	52.4	18.2	6070	US-10-204-708-9	Sequence 9, Appl
25	52.4	18.2	10619	US-10-204-708-4	Sequence 4, Appl
26	52.2	18.1	1738	US-09-918-909A-27	Sequence 27, Appl
27	52.2	18.1	3138	US-07-867-106-4	Sequence 4, Appl

c	28	52.2	18.1	6113	4	US-10-204-708-14	Sequence 14, Appl
	29	52	18.1	396	4	US-09-640-173-10	Sequence 10, Appl
	30	52	18.1	396	4	US-09-713-550-10	Sequence 10, Appl
	31	52	18.1	396	4	US-09-825-294-10	Sequence 10, Appl
	32	52	18.1	396	4	US-09-970-966-10	Sequence 10, Appl
	33	52	18.1	3440	1	US-08-471-791-27	Sequence 27, Appl
	34	52	18.1	3440	5	PCT-US91-01746-27	Sequence 27, Appl
	35	52	18.1	6265	4	US-09-129-112-3	Sequence 3, Appl
	36	51.8	18.0	4185	4	US-09-417-485D-7	Sequence 7, Appl
c	37	51.8	18.0	6243	2	US-09-056-075-1	Sequence 1, Appl
	38	51.6	17.9	473	1	US-08-764-100-16	Sequence 16, Appl
	39	51.6	17.9	473	1	US-08-764-100-16	Sequence 16, Appl
	40	51.6	17.9	3198	3	US-08-842-306B-48	Sequence 48, Appl
	41	51.6	17.9	3198	3	US-08-838-973B-48	Sequence 48, Appl
	42	51.6	17.9	3199	4	US-09-945-249-10	Sequence 10, Appl
	43	51.6	17.9	3199	4	US-09-041-990-10	Sequence 10, Appl
	44	51.6	17.9	4970	1	US-08-764-100-14	Sequence 14, Appl
	45	51.6	17.9	4970	1	US-08-764-100-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-442-054A-42
; Sequence 42, Application US/09442054A
; Patent No. 6770738
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Berg, Rolf H.
; APPLICANT: Mollegaard, Neils E.
; TITLE OF INVENTION: Higher Order Structure And Binding Of Peptide Nucleic Acids
; FILE REFERENCE: ISIS4290
; CURRENT APPLICATION NUMBER: US/09/442,054A
; PRIORITY FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 08/471,907
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/054,363
; PRIOR FILING DATE: 1993-04-26
; PRIOR APPLICATION NUMBER: PCT/ EP92/01219
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6770738el Sequence
US-09-442-054A-42

Query Match	24.7%;	Score	71.2;	DB	4;	Length	196;
Best Local Similarity	60.2%;	Pred. No.	0.00018;				
Matches	118;	Conservative	0;	Mismatches	78;	Indels	0;
						Gaps	0;
Qy	34	AAAGAGAGAGTAAATGAAAAAGAAAAAGAGCTTCACGAATTAGAGAAAAATATAAAAGA	93				
Db	1	AAA	60				
Qy	94	ATCGAGAGAGAACTAAATTAATTAATAAAGAGGTATAGTATAATACCTCTTCTTTTTT	153				
Db	61	AAA	120				
Qy	154	TAAGTGGCTTAAATGATTTTAGAGCTTCATTTTTTTTCACTTTTCTTTTCTTCCT	213				
Db	121	TTT	180				
Qy	214	TTTCTATATCTTTTTT	229				
Db	181	TTTTTTTTTTTTTTTTT	196				

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 304.828 Seconds
(without alignments)
4959.634 Million cell updates/sec

Title: US-09-747-385-6_COPY_5600_5887

Perfect score: 288

Sequence: 1 agtcaatcaaaaaataataa.....atcatctaaatctttaatt 288

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	84.4	29.3	435	4	AAI82079 Human pol
2	75.8	26.3	10039	6	ABL34042 Human imm
3	72.8	25.3	380	4	AAI80354 Human pol
4	72.6	25.2	585	5	ABV58085 Human pro
5	69.8	24.2	5908	4	AA545386 Chemical
6	69.8	24.2	5908	6	ABK28231 DNA trans
7	69.8	24.2	5908	6	AA561216 Human gen
8	69.6	24.2	6486	6	ABQ67050 Human ang
9	69	24.0	364	4	AAI84912 Human pol
10	68.2	23.7	433	9	ACH17038 Human imm
11	67.2	23.3	8946	6	ABL32910 Human imm
12	66.8	23.2	317	8	ABX37534 Bovine ES
13	66.6	23.1	361	4	AAI85935 Human pol
14	66.6	23.1	510	5	ABV58114 Human pro
15	66.4	23.1	461	5	ADL43834 Human ova
16	66.2	23.0	423	9	ACH19935 Human adu
17	66	22.9	6436	6	ABL32681 Human imm
18	65.8	22.8	1543	8	AC72157 Human NOV
19	65.8	22.8	6162	8	ABK31331 Signal tr
20	65.4	22.7	317	5	ABV58181 Human pro
21	65.4	22.7	603	5	ABV58645 Human pro

C 22	65.4	22.7	12138	6	ABK40033	Human che
C 23	65.4	22.7	12138	6	ABL33628	Human imm
C 24	64.4	22.3	6171	6	ABL32789	Human imm
C 25	64.2	22.3	8056	8	ABZ10100	Haematopo
C 26	64	22.2	5753	6	ABQ67116	Human ang
C 27	64	22.2	50000	6	ABL55644	AmEPV gen
C 28	63.2	21.9	6112	6	ABL32663	Human imm
C 29	63.2	21.9	21537	6	ABL33999	Human imm
C 30	62.8	21.8	3101	2	AAQ02047	Sequence
C 31	62.8	21.8	3744	3	AAA70149	Plasmodiu
C 32	62.8	21.8	9095	6	ABQ67061	Human ang
C 33	62.6	21.7	461	9	ACH28231	Human adu
C 34	62.6	21.7	8056	8	ABZ10246	Haematopo
C 35	62.4	21.7	700	4	AAH93026	Human inf
C 36	62.4	21.7	6025	4	AA545339	Chemical
C 37	62.4	21.7	6057	6	ABL31397	Signal tr
C 38	62.4	21.7	6057	6	ABL70362	Chemical
C 39	62.2	21.6	324	4	AAI82686	Human pol
C 40	62.2	21.6	419	4	AAI89272	Human pol
C 41	62	21.5	6577	6	ABL33356	Human imm
C 42	62	21.5	6577	6	ABL70561	Chemical
C 43	62	21.5	6577	6	AA561221	Human gen
C 44	61.8	21.5	480	9	ACH25001	Human adu
C 45	61.6	21.4	461	5	ADL43834	Human ova

ALIGNMENTS

RESULT 1

AAI82079	AAI82079 standard; cDNA; 435 BP.
XX	
AC	AAI82079;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human polynucleotide SEQ ID NO 2139.
XX	
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;
KW	nervous system disorders; arthritis; inflammation; ss.
OS	Homo sapiens.
XX	
FN	WO200164835-A2.
XX	
PD	07-SEP-2001.
XX	
PF	26-FEB-2001; 2001WO-US004927.
XX	
PR	28-FEB-2000; 2000US-00515126.
PR	18-MAY-2000; 2000US-00577409.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
FI	Tang YT, Liu C, Drmanac RT;
XX	
DR	WPI; 2001-514838/56.
DR	P-PSDB; AAO02148.
XX	
PT	Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT	and treating e.g. leukemia, inflammation and immune disorders.
XX	
PS	Claim 1; SEQ ID NO 2139; 1399pp + Sequence Listing; English.
XX	
CC	The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC	the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC	cytokine, cell proliferation or cell differentiation or which may induce
CC	production of other cytokines in other cell populations. The
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC	peptide therapy. The polypeptides have various cytokine-like activities,

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 1399.17 Seconds
(without alignments)
9733.921 Million cell updates/sec

Title: US-09-747-385-6_COPY_5600_5887

Perfect score: 288

Sequence: 1 agtcaatcaaaaaataataa.....atcatctaaattcttaatt 288

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	288	100.0	5887	1	AF159249
2	284.8	98.9	6281	1	AF022647
3	81.2	28.2	38692	3	AC116919
4	80.2	27.8	333321	3	AC116986
5	78.8	27.4	88549	3	AC116924
6	78.4	27.2	105682	3	AC116957_3
7	77.6	26.9	110000	3	AC116957_0
8	77.4	26.9	302156	3	AC116977
9	77	26.7	156975	2	CR394534
10	76.2	26.5	110000	3	AC116984_1
11	76.2	26.5	349980	6	AX344566
12	76	26.4	2781	3	AY044085
13	75.8	26.3	10039	6	AX346944
14	75.8	26.3	125623	3	AC115599
15	75.8	26.3	266544	3	AC116956
16	75.8	26.3	273275	3	AE014828
17	75.4	26.2	105320	3	AC116920
18	75.4	26.2	178273	2	AC005308
19	75.4	26.2	250531	3	AE014845

20	75.2	26.1	192187	3	AC117072
21	74.8	26.0	156978	2	CR339045
22	74.4	25.8	132254	3	AC116330
23	73.8	25.6	7554	3	AY160096
24	73.8	25.6	125623	3	AC115599
25	73.8	25.6	182870	3	AC116960
26	73.6	25.6	88549	3	AC116924
27	73.4	25.5	253305	3	PFMAL387
28	73.2	25.4	4951	3	AY160092
29	73.2	25.4	110000	3	AC116957_0
30	73.2	25.4	250029	3	AE014838
31	73	25.3	61052	2	AC123513
32	73	25.3	136240	3	AC117070
33	72.8	25.3	4430	3	AY160097
34	72.8	25.3	40611	3	AC116987
35	72.8	25.3	105320	3	AC116920
36	72.8	25.3	110000	3	AC116305_3
37	72.8	25.3	192187	3	AC117072_3
38	72.6	25.2	585	6	CQ526237
39	72.6	25.2	4000	3	AF482963
40	72.6	25.2	133426	2	AC134521
41	72.6	25.2	349751	3	PFMAL4P3
42	72.4	25.1	1504	3	DDH4
43	72.2	25.1	182871	3	AC117176
44	72	25.0	39838	2	AC149329
45	72	25.0	110000	2	PFMAL7P1_06

ALIGNMENTS

RESULT 1	AF159249	AF159249	5887 bp	DNA	circular BCT 09-FEB-2000
LOCUS	Fusobacterium nucleatum plasmid pFN1	AF159249			complete sequence.
DEFINITION	Fusobacterium nucleatum plasmid pFN1	AF159249.1	GI:6941824		
ACCESSION	Fusobacterium nucleatum				
VERSION	Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;				
KEYWORDS	Fusobacterium				
SOURCE	1 (bases 1 to 5887)				
REFERENCE	Kinder Haake,S. and Finegold,S.M.				
AUTHORS	DNA sequence analysis of the Fusobacterium nucleatum plasmid, pFN1				
TITLE	J. Dent. Res. 78, 420 (1999)				
JOURNAL	2 (bases 1 to 5887)				
REFERENCE	Kinder Haake,S. and Yoder,S.				
AUTHORS	Transformation of Fusobacterium nucleatum by electroporation				
TITLE	(Abstract #H-9)				
JOURNAL	Abstr. Gen. Meet. Am. Soc. Microbiol. 99, 331 (1999)				
REFERENCE	3 (bases 1 to 5887)				
AUTHORS	Haake,S.K., Yoder,S.C., Attarian,G. and Podkaminer,K.				
TITLE	Native plasmids of Fusobacterium nucleatum: characterization and use in development of genetic systems				
JOURNAL	J. Bacteriol. 182 (4), 1176-1180 (2000)				
REFERENCE	20115567				
PUBMED	10648549				
REFERENCE	4 (bases 1 to 5887)				
AUTHORS	Kinder Haake,S.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-JUN-1999) Periodontics, UCLA School of Dentistry,				
FEATURES	10833 LeConte Avenue, Los Angeles, CA 90095-1668, USA				
source	Location/Qualifiers				
	1. 5887				
	/organism="Fusobacterium nucleatum"				
	/mol_type="genomic DNA"				
	/strain="12230"				
	/db_xref="taxon:851"				
	/plasmid="pFN1"				
	/notes="lower-respiratory tract clinical isolate from the Wadsworth Anaerobe Laboratory, West Los Angeles Veterans Affairs Medical Center"				

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 12:44:02 ; Search time 1141.04 Seconds
(without alignments)
1237.519 Million cell updates/sec

Title: US-09-747-385-6_COPY_1_250
Perfect score: 250
Sequence: 1 catataataactttttgttt.....agccataataataaaaat 250

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09D_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	31.2	499	17	US-10-021-323-10189
2	77.6	31.0	594	16	US-10-424-599-116262
3	74.2	29.7	560	17	US-10-021-323-2253
4	73.2	29.3	469	17	US-10-021-323-16830
5	73.2	29.3	520	17	US-10-021-323-7699
6	73.2	29.3	528	17	US-10-021-323-8131
7	73.2	29.3	560	17	US-10-021-323-2253
8	72.8	29.1	499	17	US-10-021-323-10189
9	72.6	29.0	469	17	US-10-021-323-16830
10	72.6	29.0	520	17	US-10-021-323-7699
11	72.6	29.0	556	18	US-10-357-930-40082
12	72.6	29.0	556	18	US-10-357-930-40182

c 13	72.6	29.0	556	18	US-10-357-930-42124	Sequence 42124, A
c 14	72.6	29.0	556	18	US-10-357-930-43620	Sequence 43620, A
c 15	72.6	29.0	626	18	US-10-357-930-60960	Sequence 60960, A
c 16	72	28.8	277	9	US-09-960-352-12673	Sequence 12673, A
c 17	72	28.8	433	17	US-10-021-323-6681	Sequence 6681, Ap
c 18	71.8	28.7	487	17	US-10-021-323-2841	Sequence 2841, Ap
c 19	71.6	28.6	309	18	US-10-357-930-45013	Sequence 45013, A
c 20	71.6	28.6	353	17	US-10-021-323-8039	Sequence 8039, Ap
c 21	70.2	28.1	375	18	US-10-357-930-44930	Sequence 44930, Ap
c 22	70	28.0	565	17	US-10-021-323-11125	Sequence 11125, A
c 23	68.6	27.4	486	17	US-10-021-323-6536	Sequence 6536, Ap
c 24	68.6	27.4	547	17	US-10-021-323-6195	Sequence 6195, Ap
c 25	68.4	27.4	398	17	US-10-021-323-7863	Sequence 7863, Ap
c 26	68.4	27.4	565	17	US-10-021-323-11125	Sequence 11125, A
c 27	68.2	27.3	9095	17	US-10-433-793-91	Sequence 91, Appl
c 28	68	27.2	534	17	US-10-021-323-13500	Sequence 13500, A
c 29	67.8	27.1	277	9	US-09-960-352-12673	Sequence 12673, A
c 30	67.8	27.1	319	17	US-10-021-323-7947	Sequence 7947, Ap
c 31	67.8	27.1	428	17	US-10-021-323-7700	Sequence 7700, Ap
c 32	67.8	27.1	526	17	US-10-021-323-14764	Sequence 14764, A
c 33	67.8	27.1	537	17	US-10-021-323-8120	Sequence 8120, Ap
c 34	67.2	26.9	762	16	US-10-424-599-34277	Sequence 34277, A
c 35	67	26.8	419	9	US-09-960-352-11234	Sequence 11234, A
c 36	67	26.8	547	17	US-10-021-323-16890	Sequence 16890, A
c 37	67	26.8	574	17	US-10-021-323-11147	Sequence 11147, Ap
c 38	66.8	26.7	467	17	US-10-021-323-6541	Sequence 6541, Ap
c 39	66.8	26.7	516	17	US-10-021-323-6457	Sequence 6457, Ap
c 40	66.8	26.7	516	17	US-10-021-323-16996	Sequence 16996, A
c 41	66.8	26.7	517	17	US-10-021-323-11054	Sequence 11054, A
c 42	66.8	26.7	529	17	US-10-021-323-10810	Sequence 10810, A
c 43	66.8	26.7	1533	18	US-10-723-860-7968	Sequence 7968, Ap
c 44	66.8	26.7	3673778	15	US-10-312-841-1	Sequence 1, Appl
c 45	66.6	26.6	299	10	US-09-814-353-4844	Sequence 4844, Ap

ALIGNMENTS

RESULT 1

US-10-021-323-10189
; Sequence 10189, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Ziegler, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 10189
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3828-023-Q6-N6-C10

Query Match 31.2%; Score 78; DB 17; Length 499;
Best Local Similarity 58.0%; Pred. No. 0.0014;
Matches 138; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy	12	TTTTGTTCTCTCTAGTACTTTTTTCTAACTTTTAACTTTTCTTTTACTTTTT	71
Db	42	TT	101
Qy	72	TCAATTTTTCTAATCAATCGCTTTTAACTTTCTTAAAGCTTTTAAATTTTTTAGTA	131

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 56.0345 Seconds
(without alignments)
3171.212 Million cell updates/sec

Title: US-09-747-385-6_COPY_1_250

Perfect score: 250

Sequence: 1 catataataactttttgttt.....agccataataataaaaaa 250

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A-COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B-COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A-COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B-COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS-COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	63	25.2	2447	2	US-09-014-969-14
c 2	61.6	24.6	396	4	US-09-640-173-53
c 3	61.6	24.6	396	4	US-09-713-550-53
c 4	61.6	24.6	396	4	US-09-825-294-53
c 5	61.6	24.6	396	4	US-09-970-966-53
c 6	61.2	24.5	1738	4	US-09-918-909A-27
c 7	59.2	23.7	240	1	US-08-628-417-6
c 8	58.2	23.3	1447	4	US-09-443-041A-27
c 9	57.6	23.0	441	4	US-09-601-537-10
c 10	57.6	23.0	441	4	US-09-601-537-9
c 11	57.2	22.9	4121	4	US-09-311-021-171
c 12	57.2	22.8	1474	3	US-08-821-994-64
c 13	57	22.6	2146	4	US-10-003-392-3
c 14	56.8	22.7	6152	4	US-10-204-708-47
c 15	56.6	22.6	5152	4	US-09-640-173-33
c 16	56.2	22.5	396	4	US-09-713-550-33
c 17	56.2	22.5	396	4	US-09-825-294-33
c 18	56.2	22.5	396	4	US-09-970-966-33
c 19	56.2	22.5	396	4	US-09-970-966-33
c 20	56.2	22.5	1696	4	US-09-835-811-1
c 21	56	22.4	6409	4	US-09-967-908A-1
c 22	56	22.4	6409	4	US-10-159-151-1
c 23	55.8	22.3	7724	4	US-08-486-049-1
c 24	55.6	22.2	1117	3	US-09-247-373B-33
c 25	55.4	22.2	1985	4	US-09-907-794A-212
c 26	55.4	22.2	1985	4	US-09-905-125A-212
c 27	55.4	22.2	1985	4	US-09-902-775A-212

c 28	55.4	22.2	1985	4	US-09-906-700-212	Sequence 212, Appl
c 29	55.4	22.2	1985	4	US-09-903-603A-212	Sequence 212, Appl
c 30	55	22.0	2394	4	US-09-800-729-33	Sequence 33, Appl
c 31	55	22.0	2476	4	US-10-140-002-489	Sequence 489, Appl
c 32	55	22.0	11050	4	US-10-204-708-86	Sequence 86, Appl
c 33	54.4	21.8	359	4	US-09-621-976-16019	Sequence 16019, A
c 34	54	21.6	1020	4	US-09-328-475C-43	Sequence 43, Appl
c 35	54	21.6	1052	4	US-09-489-847-23	Sequence 23, Appl
c 36	53.8	21.5	359	4	US-09-621-976-16008	Sequence 16008, A
c 37	53.8	21.5	362	4	US-09-621-976-16010	Sequence 16010, A
c 38	53.8	21.5	365	4	US-09-621-976-16042	Sequence 16042, A
c 39	53.8	21.5	708	4	US-09-270-767-13081	Sequence 13081, A
c 40	53.8	21.5	3275	4	US-09-370-838-151	Sequence 151, Appl
c 41	53.8	21.5	3275	4	US-09-854-133-151	Sequence 151, Appl
c 42	53.6	21.4	2434	4	US-09-489-847-67	Sequence 67, Appl
c 43	53.6	21.4	2527	4	US-09-244-805-29	Sequence 29, Appl
c 44	53.4	21.4	1798	3	US-09-797-906-1	Sequence 1, Appl
c 45	53.2	21.3	1733	3	US-09-073-569-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-014-969-14/c
; Sequence 14, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,969
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-014-969-14

Query Match 25.2%; Score 63; DB 2; Length 2447;
Best Local Similarity 57.5%; Pred. No. 0.0014;
Matches 111; Conservative 1; Mismatches 81; Indels 0; Gaps 0;

Result No.	Query %			Length	DB	ID	Description
	Score	Match	Length				
C 1	72.6	29.0	556	5	ABV40163	Abv40163	Human pro
C 2	72.6	29.0	556	5	ABV40063	Abv40063	Human pro
C 3	72.6	29.0	556	5	ABV42105	Abv42105	Human pro
C 4	72.6	29.0	556	5	ABV43601	Abv43601	Human pro
C 5	72.6	29.0	626	5	ABV60941	Abv60941	Human pro
C 6	72	28.8	277	8	ABX47508	Abx47508	Bovine ES
C 7	71.6	28.6	309	5	ABV44994	Abv44994	Human pro
C 8	70.2	28.1	375	5	ABV44911	Abv44911	Human pro
C 9	70.2	28.1	774	10	ADK57243	Adk57243	Plant DNA
C 10	68.2	27.3	9095	6	ABQ67061	Abq67061	Human ang
C 11	67.8	27.1	277	8	ABX47508	Abx47508	Bovine ES
C 12	67	26.8	310	4	AHx71505	Ahx71505	Human cer
C 13	67	26.8	419	8	ABX46069	Abx46069	Bovine ES
C 14	66.8	26.7	1533	12	ADQ25148	Adq25148	Human sof
C 15	66.6	26.6	299	5	ADI72102	Adi72102	Human ova
C 16	66.6	26.6	299	5	ADL37251	Adl37251	Human ova
C 17	66.6	26.6	626	5	ABV60941	Abv60941	Human pro
C 18	66.6	26.6	2427	2	AAQ04107	Aaq04107	Human pro
C 19	65.8	26.3	545	4	AHx70126	Ahx70126	Human cer
C 20	65.8	26.3	621	4	AAH71551	Aah71551	Human cer
C 21	65.6	26.2	494	5	ABV10021	Abv10021	Human pro

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 1214.56 Seconds
(without alignments)
9733.921 Million cell updates/sec

Title: US-09-747-385-6_COPY_1_250

Perfect score: 250

Sequence: 1 catataataactttttgttt.....agccataataataaaaaa 250

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	250	100.0	5887	1	AF159249	AF159249 Fusobacte
2	223	89.2	6281	1	AF022647	AF022647 Fusobacte
C 3	72.6	29.0	556	6	CQ508215	Sequence
C 4	72.6	29.0	556	6	CQ508315	Sequence
C 5	72.6	29.0	556	6	CQ510257	Sequence
C 6	72.6	29.0	556	6	CQ511753	Sequence
C 7	72.6	29.0	626	6	CQ529093	Sequence
8	71.8	28.7	227273	2	AC141526	Rattus no
C 9	71.6	28.6	309	6	CQ513146	Sequence
C 10	71.2	28.5	177560	2	CR318627	Danio rer
11	70.8	28.3	129518	2	AC149940	Strongylo
12	70.2	28.1	375	6	CQ513063	Sequence
13	69.8	27.9	202872	2	AC016160	Homo sapi
14	69.4	27.8	110000	3	AC116984	Continuation (2 of
C 15	69.2	27.7	1373	10	BC049731	Mus muscu
C 16	69.2	27.7	1930	5	BC066725	Danio rer
17	69	27.6	182871	3	AC117176	Dictyoste
C 18	68.8	27.5	218404	5	BX470087	Zebrafish
C 19	68.6	27.4	1946	5	BC077411	Xenopus 1

20	68.4	27.4	195422	2	CR450745	Danio rer
21	68.2	27.3	9095	6	AX458545	Sequence
C 22	67.8	27.1	2005	9	HSM803426	AL832119 Homo sapi
23	67.6	27.0	195057	2	BX897664	Danio rer
24	67.4	27.0	134597	2	CR391983	Danio rer
C 25	67.2	26.9	88549	3	AC116924	Dictyoste
C 26	67.2	26.9	343050	3	PFA929353	Plasmodiu
27	67	26.8	310	6	AX187085	Sequence
28	67	26.8	57203	3	AC115581	Dictyoste
29	66.8	26.7	90373	3	AC115680	Dictyoste
C 30	66.8	26.7	146570	3	AC117076	Dictyoste
C 31	66.8	26.7	180665	2	CR382366	Danio rer
32	66.8	26.7	349980	6	AX344559	Sequence
33	66.6	26.6	299	6	CQ397773	Sequence
34	66.6	26.6	299	6	CQ404070	Sequence
35	66.6	26.6	626	6	CQ529093	Sequence
C 36	66.6	26.6	192525	2	BX936428	Danio rer
37	66.6	26.6	192955	2	AC148921	Callithri
C 38	66.2	26.5	2725	5	BC077764	Xenopus 1
39	66.2	26.5	194883	2	CR450839	Danio rer
C 40	66.2	26.5	211748	2	CR392346	Danio rer
C 41	66	26.4	1606	10	BC051176	Mus muscu
42	66	26.4	57538	3	AC115682	Dictyoste
C 43	66	26.4	90373	3	AC115680	Dictyoste
44	65.8	26.3	545	6	AX185705	Sequence
45	65.8	26.3	621	6	AX187131	Sequence

ALIGNMENTS

RESULT 1	AF159249	Fusobacterium nucleatum plasmid pFN1, complete sequence.	5887 bp	DNA	circular BCT 09-FEB-2000
LOCUS	AF159249	AF159249.1	GI:6941824		
DEFINITION	Fusobacterium nucleatum				
ACCESSION	AF159249				
VERSION	AF159249.1				
KEYWORDS	Fusobacterium nucleatum				
SOURCE	Fusobacterium nucleatum				
ORGANISM	Fusobacterium nucleatum				
REFERENCE	1 (bases 1 to 5887)				
AUTHORS	Kinder Haake, S. and Finegold, S.M.				
TITLE	DNA sequence analysis of the Fusobacterium nucleatum plasmid, pFN1				
JOURNAL	J. Dent. Res. 78, 420 (1999)				
REFERENCE	2 (bases 1 to 5887)				
AUTHORS	Kinder Haake, S. and Yoder, S.				
TITLE	Transformation of Fusobacterium nucleatum by electroporation				
JOURNAL	Abstr. Gen. Meet. Am. Soc. Microbiol. 99, 331 (1999)				
REFERENCE	3 (bases 1 to 5887)				
AUTHORS	Haake, S.K., Yoder, S.C., Attarian, G. and Podkaminer, K.				
TITLE	Native plasmids of Fusobacterium nucleatum: characterization and use in development of genetic systems				
JOURNAL	J. Bacteriol. 182 (4), 1176-1180 (2000)				
REFERENCE	20115567				
PUBMED	10648549				
REFERENCE	4 (bases 1 to 5887)				
AUTHORS	Kinder Haake, S.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-JUN-1999) Periodontics, UCLA School of Dentistry, 10833 LeConce Avenue, Los Angeles, CA 90095-1668, USA				
FEATURES	Location/Qualifiers				
source	1. 5887				
	/organism="Fusobacterium nucleatum"				
	/mol_type="genomic DNA"				
	/strain="12230"				
	/db_xref="taxon:851"				
	/plasmid="pFN1"				
	/notes="lower-respiratory tract clinical isolate from the Wadsworth Anaerobe Laboratory, West Los Angeles Veterans Affairs Medical Center"				

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 2249.52 Seconds
(without alignments)
4049.721 Million cell updates/sec

Title: US-09-747-385-15_COPY_1_250

Perfect score: 250

Sequence: 1 cacctgacgcgcctgtacg.....ggttcacgtagtgggccatc 250

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	250	100.0	500	6	CD451062	CD451062 USDA-FP 1
C 2	250	100.0	528	9	CG808215	CG808215 1118090D0
C 3	250	100.0	539	9	CG801749	CG801749 1118024B0
C 4	250	100.0	581	1	AV403804	AV403804 AV403804
C 5	250	100.0	584	1	AV404063	AV404063 AV404063
C 6	250	100.0	608	1	AJ611113	AJ611113 AJ611113
C 7	250	100.0	613	1	AU250522	AU250522 AU250522
C 8	250	100.0	614	5	BQ823788	BQ823788 1030112G0
C 9	250	100.0	625	5	BQ813491	BQ813491 1030036H0
C 10	250	100.0	627	1	AV403998	AV403998 AV403998
C 11	250	100.0	627	1	AV404060	AV404060 AV404060
C 12	250	100.0	627	1	AV404091	AV404091 AV404091
C 13	250	100.0	627	1	AV404095	AV404095 AV404095
C 14	250	100.0	628	1	AV403779	AV403779 AV403779
C 15	250	100.0	628	1	AV403828	AV403828 AV403828
C 16	250	100.0	628	1	AV403918	AV403918 AV403918
C 17	250	100.0	628	1	AV403919	AV403919 AV403919
C 18	250	100.0	628	1	AV403945	AV403945 AV403945
C 19	250	100.0	628	1	AV403970	AV403970 AV403970
C 20	250	100.0	628	1	AV403997	AV403997 AV403997
C 21	250	100.0	628	1	AV404068	AV404068 AV404068
C 22	250	100.0	629	1	AV404061	AV404061 AV404061
C 23	250	100.0	630	5	BQ819966	BQ819966 1030081D0
C 24	250	100.0	642	7	CN582805	CN582805 USDA-FP_1

C 25	250	100.0	659	1	AU251092	AU251092 AU251092
C 26	250	100.0	660	1	AU248437	AU248437 AU248437
C 27	250	100.0	660	5	BQ814002	BQ814002 1030040D0
C 28	250	100.0	661	1	AU249975	AU249975 AU249975
C 29	250	100.0	663	7	CO641266	CO641266 USDA-FP_1
C 30	250	100.0	665	1	AU247386	AU247386 AU247386
C 31	250	100.0	666	6	CB550392	CB550392 MMPL0002
C 32	250	100.0	667	6	CB550481	CB550481 MMPL0002
C 33	250	100.0	676	6	CB549779	CB549779 MMPL0018
C 34	250	100.0	681	1	AV403811	AV403811 AV403811
C 35	250	100.0	681	1	AV403921	AV403921 AV403921
C 36	250	100.0	681	6	CB548636	CB548636 MMPL0018
C 37	250	100.0	683	6	CB550005	CB550005 MMPL0006
C 38	250	100.0	684	1	AV404405	AV404405 AV404405
C 39	250	100.0	685	5	BU724260	BU724260 SJMBFC05
C 40	250	100.0	689	1	AU249799	AU249799 AU249799
C 41	250	100.0	689	5	BQ819196	BQ819196 1030076B0
C 42	250	100.0	690	1	AU246979	AU246979 AU246979
C 43	250	100.0	690	1	AV405131	AV405131 AV405131
C 44	250	100.0	695	6	CB550355	CB550355 MMPL0003
C 45	250	100.0	696	6	CB549815	CB549815 MMPL0011

ALIGNMENTS

RESULT 1
CD451062/c
LOCUS CD451062 500 bp mRNA linear EST 03-JUN-2003
DEFINITION USDA-FP 103109 Adult Alate Brown Citrus Aphid Toxoptera citricida
cDNA clone WHWC-41_F12 5', mRNA sequence.
ACCESSION CD451062
VERSION CD451062.1 GI:31365802
KEYWORDS EST.
SOURCE Toxoptera citricida (brown citrus aphid)
ORGANISM Toxoptera citricida
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Aphidini; Toxoptera.
REFERENCE 1 (bases 1 to 500)
HUNTER, W.B., DANG, P.M., BAUSHER, M.G., CHAPARRO, J.X., MCKENDREE, W.,
SHATTERS, R.G. JR., MCKENZIE, C.L. and SINISTERA, X.H.
Aphid biology: Expressed genes from alate Toxoptera citricida, the
brown citrus aphid
J. Insect Sci. 3 (23), 1-7 (2003)
COMMENT Contact: Wayne B. Hunter
US Horticultural Research Laboratory
USDA - ARS
2001 South Rock Rd., Fort Pierce, FL 34945, USA
Tel: (772) 462-5898
Fax: (772) 462-5986
Email: whunter@ushrl.ars.usda.gov
Seq primer: T3 Primer.
Location/Qualifiers
source 1..500
/organism="Toxoptera citricida"
/mol_type="mRNA"
/db_xref="taxon:223852"
/clone="WHWC-41_F12"
/sex="Mixed population"
/tissue_type="Entire insect"
/dev_stage="Adult Alate"
/lab_host="XLI-Blue"
/clone_lib="Adult Alate Brown Citrus Aphid"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; Toxoptera citricida (Kirkaldy); A high quality EST
with at least 100 contiguous bases at Trace Tuner score of
20 or better."

Query Match 100.0%; Score 250; DB 6; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.5e-62;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 12:44:02 ; Search time 1141.04 Seconds
(without alignments)
1237.519 Million cell updates/sec

Title: US-09-747-385-15_COPY_1_250

Perfect score: 250

Sequence: 1 caccgtacgcgcctctagc.....ggttcacgtagtgggccatc 250

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	250	100.0	3327	17	US-10-796-486-56
2	250	100.0	3369	17	US-10-796-486-56
3	250	100.0	3379	15	US-10-222-026A-19
4	250	100.0	3417	17	US-10-466-959-1
5	250	100.0	3417	18	US-10-466-960A-1
6	250	100.0	3450	15	US-10-222-026A-20
7	250	100.0	3497	16	US-10-420-529-11
8	250	100.0	3501	17	US-10-466-959-2
9	250	100.0	3501	18	US-10-466-960A-2
10	250	100.0	3621	17	US-10-471-607-11
11	250	100.0	3954	17	US-10-796-486-53
12	250	100.0	3954	17	US-10-796-486-57

13	250	100.0	3976	17	US-10-796-486-49
14	250	100.0	3988	15	US-10-393-269-12
15	250	100.0	4151	16	US-10-421-285-15
16	250	100.0	4188	17	US-10-466-959-3
17	250	100.0	4188	18	US-10-466-960A-3
18	250	100.0	4390	9	US-09-968-355-18
19	250	100.0	4412	18	US-10-677-777-3
20	250	100.0	4438	9	US-09-968-355-21
21	250	100.0	4516	9	US-09-968-355-24
22	250	100.0	4594	9	US-09-968-355-15
23	250	100.0	4665	9	US-09-759-960-7
24	250	100.0	4665	18	US-10-603-062-7
25	250	100.0	4677	15	US-10-237-146-7
26	250	100.0	4692	15	US-10-161-403-29
27	250	100.0	4692	17	US-10-433-640-16
28	250	100.0	4727	15	US-10-115-987B-12
29	250	100.0	4733	10	US-09-797-496B-1
30	250	100.0	4733	15	US-10-177-390-1
31	250	100.0	4740	15	US-10-115-987B-13
32	250	100.0	4748	10	US-09-796-575-4
33	250	100.0	4748	17	US-10-652-814-4
34	250	100.0	4778	15	US-10-138-998A-1
35	250	100.0	4782	15	US-10-138-998A-2
36	250	100.0	4793	18	US-10-737-290-141
37	250	100.0	4862	15	US-10-161-403-87
38	250	100.0	4883	14	US-10-006-593-111
39	250	100.0	4883	15	US-10-307-724-111
40	250	100.0	4883	18	US-10-737-290-111
41	250	100.0	4886	14	US-10-128-853-4
42	250	100.0	4894	14	US-10-055-794-2
43	250	100.0	4943	13	US-10-001-189-54
44	250	100.0	4944	13	US-10-001-189-55
45	250	100.0	4944	13	US-10-001-189-56

ALIGNMENTS

RESULT 1
US-10-796-486-56
; Sequence 56, Application US/10796486
; Publication No. US20040171574A1
; GENERAL INFORMATION:
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE
; FILE REFERENCE: PC10525B
; CURRENT APPLICATION NUMBER: US/10/796.486
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/09/628.730
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 3327
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pGHRH1-29Yalal522SK construct
US-10-796-486-56

Query Match	100.0%;	Score 250;	DB 17;	Length 3327;
Best Local Similarity	100.0%;	Pred. No. 2.5e-73;		
Matches 250;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CACCTGACGGCCCTGTAGCGCGCATTTAAGCGCGCGGGTGTGTGTGTACGCGCAGCG	60	
Db	2575	CACCTGACGGCCCTGTAGCGCGCATTTAAGCGCGCGGGTGTGTGTGTACGCGCAGCG	2634	
QY	61	TGACCGGTACACTTTCGACGGCCCTAGCGCCGCTCCTTTTCGCTTCTTCCCTTCCTTTC	120	
Db	2635	TGACCGGTACACTTTCGACGGCCCTAGCGCCGCTCCTTTTCGCTTCTTCCCTTCCTTTC	2694	

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 56.0345 Seconds
(without alignments)
3171.212 Million cell updates/sec

Title: US-09-747-385-15_COPY_1_250

Perfect score: 250

Sequence: 1 caccctgacgcgcctgtacg.....gggtcacgtagtggccatc 250

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A-COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B-COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A-COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B-COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS-COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250	100.0	3327	4	US-09-628-730-56
2	250	100.0	3369	4	US-09-628-730-48
3	250	100.0	3379	4	US-09-318-786-19
4	250	100.0	3450	4	US-09-318-786-20
5	250	100.0	3456	1	US-08-232-463-8
6	250	100.0	3688	1	US-08-232-463-9
7	250	100.0	3878	3	US-08-651-472-65
8	250	100.0	3878	3	US-08-358-928-65
9	250	100.0	3954	4	US-09-628-730-53
10	250	100.0	3954	4	US-09-628-730-57
11	250	100.0	3976	4	US-09-628-730-49
12	250	100.0	3988	4	US-09-358-856C-12
13	250	100.0	4435	2	US-08-792-824-1
14	250	100.0	4518	4	US-09-380-190A-26
15	250	100.0	4659	1	US-08-232-463-10
16	250	100.0	4665	3	US-08-948-378A-7
17	250	100.0	4665	3	US-09-169-425C-7
18	250	100.0	4665	4	US-09-759-960-7
19	250	100.0	4691	3	US-08-591-632-43
20	250	100.0	4691	3	US-09-611-451-43
21	250	100.0	4701	3	US-08-651-472-64
22	250	100.0	4701	3	US-08-358-928-64
23	250	100.0	4748	4	US-09-796-575-4
24	250	100.0	4818	1	US-08-232-463-11
25	250	100.0	4821	1	US-08-232-463-12
26	250	100.0	4824	1	US-08-232-463-13
27	250	100.0	4886	4	US-09-533-220A-4

c	28	250	100.0	4992	4	US-09-796-575-5	Sequence 5, Appli
	29	250	100.0	4997	1	US-08-232-463-1	Sequence 1, Appli
c	30	250	100.0	5069	4	US-09-393-483A-1	Sequence 1, Appli
	31	250	100.0	5069	4	US-09-393-483A-2	Sequence 2, Appli
	32	250	100.0	5163	4	US-09-628-730-54	Sequence 54, Appli
	33	250	100.0	5281	4	US-09-921-263-1	Sequence 1, Appli
	34	250	100.0	5283	4	US-09-628-730-58	Sequence 58, Appli
	35	250	100.0	5325	4	US-09-628-730-50	Sequence 50, Appli
c	36	250	100.0	5532	4	US-08-961-888-40	Sequence 40, Appli
	37	250	100.0	5789	3	US-08-862-431-32	Sequence 32, Appli
	38	250	100.0	5791	3	US-08-862-431-31	Sequence 31, Appli
	39	250	100.0	5793	3	US-08-862-431-29	Sequence 29, Appli
	40	250	100.0	5793	3	US-08-862-431-30	Sequence 30, Appli
	41	250	100.0	5818	2	US-08-536-559A-3	Sequence 3, Appli
	42	250	100.0	5819	2	US-08-536-559A-2	Sequence 2, Appli
	43	250	100.0	5819	3	US-08-862-431-27	Sequence 27, Appli
	44	250	100.0	5819	3	US-08-862-431-28	Sequence 28, Appli
	45	250	100.0	5909	4	US-09-921-263-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-628-730-56
; Sequence 56, Application US/09628730
; Patent No. 6759393
; GENERAL INFORMATION:
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE
; FILE REFERENCE: PC10525B
; CURRENT APPLICATION NUMBER: US/09/628,730
; CURRENT FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 3327
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pGHRH1-29Yala1522SK construct
US-09-628-730-56

Query Match 100.0%; Score 250; DB 4; Length 3327;
Best Local Similarity 100.0%; Pred. No. 1.1e-64;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CACCTGACGGCCCTGTAGCGGCGCATTAAGCGCGCGGTGTGGTGTACGGCGAGCG	60
Db	2575	CACCTGACGGCCCTGTAGCGGCGCATTAAGCGCGCGGTGTGGTGTACGGCGAGCG	2634
Qy	61	TGACCGGTACACTTGCCAGCGCCCTAGCGCGCGCTCTTCGCTTTCTCCCTTCCTTTC	120
Db	2635	TGACCGGTACACTTGCCAGCGCCCTAGCGCGCGCTCTTCGCTTTCTCCCTTCCTTTC	2694
Qy	121	TGCGCAGTTTCGCGCGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTTC	180
Db	2695	TGCGCAGTTTCGCGCGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTTC	2754
Qy	181	GATTAGTGTCTTACGGCACCTCGACCCCAAAAACCTTGATGGGTGATGGTTCACGTA	240
Db	2755	GATTAGTGTCTTACGGCACCTCGACCCCAAAAACCTTGATGGGTGATGGTTCACGTA	2814
Qy	241	GTGGGCCATC	250
Db	2815	GTGGGCCATC	2824

RESULT 2

US-09-628-730-48
; Sequence 48, Application US/09628730

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 264.607 Seconds
(without alignments)
4959.634 Million cell updates/sec

Title: US-09-747-385-15_COPY_1_250

Perfect score: 250

Sequence: 1 caccctgagcgccctgtagc.....ggttcacgtagtgcccatc 250

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001s:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	250	100.0	2946	3	AAA75650 Nucleotid
2	250	100.0	2958	2	Aaz11648 pBluescri
3	250	100.0	3327	4	Aac86263 Plasmid G
4	250	100.0	3327	6	Abk53274 Growth ho
5	250	100.0	3369	4	Aac86255 pGHRH-4
6	250	100.0	3369	6	Abk53266 Growth ho
7	250	100.0	3379	4	Aac66992 Vector pC
8	250	100.0	3417	6	Abq74934 Entry vec
9	250	100.0	3417	6	Abk90545 Vector DN
10	250	100.0	3417	6	Aad45825 EVE4 vect
11	250	100.0	3417	6	Abk90623 DNA seque
12	250	100.0	3417	10	Adc37163 Entry vec
13	250	100.0	3417	12	Adk01056 Entry vec
C 14	250	100.0	3450	4	Aac66993 Vector pC
C 15	250	100.0	3473	8	Abz57850 Plasmid p
C 16	250	100.0	3473	8	Abz80274 Peptide-1
17	250	100.0	3501	6	Abq74935 Entry vec
18	250	100.0	3501	6	Abk90546 Vector DN
19	250	100.0	3501	6	Aad45826 EVE5 vect
20	250	100.0	3501	6	Abk90624 DNA seque
21	250	100.0	3501	10	Adc37164 Entry vec

C 22	250	100.0	3501	12	ADK01057
C 23	250	100.0	3621	8	ABV77131
C 24	250	100.0	3723	4	AD10000
C 25	250	100.0	3747	2	ADH11242
C 26	250	100.0	3851	12	ADP80954
C 27	250	100.0	3878	2	AAQ40299
C 28	250	100.0	3878	3	AAA89876
C 29	250	100.0	3878	4	AA12794
C 30	250	100.0	3954	4	AAC86260
31	250	100.0	3954	6	ABK53275
32	250	100.0	3954	6	ABK53271
33	250	100.0	3976	4	AAC86256
34	250	100.0	3976	6	ABK53267
35	250	100.0	3988	2	AAx87639
36	250	100.0	3988	4	AAx72857
37	250	100.0	3988	10	ADB88985
38	250	100.0	3988	12	ADJ33442
C 39	250	100.0	4055	5	AA168460
C 40	250	100.0	4151	12	ADK19677
C 41	250	100.0	4151	12	ADP03093
42	250	100.0	4163	3	AA229134
43	250	100.0	4188	6	ABQ74936
44	250	100.0	4188	6	ABK90547
45	250	100.0	4188	6	AAD45827

ALIGNMENTS

RESULT 1

AAA75650/c

ID AAA75650 standard; DNA; 2946 BP.

AC AAA75650;

DT 22-JAN-2001 (first entry)

XX Nucleotide sequence of internal control plasmid pNW35.

XX Genome genetic analysis; nucleic acid characterization; phenotype;

XX inter-population perfectly matched duplex depletion; plasmid pNW35; ss.

XX Synthetic.

PN WO200055364-A2.

PD 21-SEP-2000.

PF 10-MAR-2000; 2000WO-GB000916.

PR 12-MAR-1999; 99EP-00301933.

XX (AMSH) AMERSHAM PHARMACIA BIOTECH UK LTD.

XX Reeve MA, Workman NI, Martin-Parras L;

XX WPI; 2000-602127/57.

XX Genome analysis termed inter-population perfectly matched duplex

XX depletion, that overcomes limitations of current approach based on single

XX nucleotide polymorphism and linkage disequilibrium in isolated

XX populations.

XX Example 1b; Page 121-122; 167pp; English.

XX The specification describes method for whole genome genetic analysis. The

XX method is designated inter-population perfectly matched duplex depletion.

XX The method uses a mixture of DNA fragments enriched in fragments that are

XX characteristic of a phenotype of interest. The mixture of DNA fragments

XX is achieved by mixing fragments of affected and unaffected DNA under

XX hybridising conditions, and recovering a mixture of hybrids that contain

XX mismatches. The method is used for nucleic acid characterization. The

XX method can be also used to characterise several nucleic acid fragments of

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 1214.56 Seconds
(without alignments)
9733.921 Million cell updates/sec

Title: US-09-747-385-15_COPY_1_250

Perfect score: 250

Sequence: 1 caccctgacgcgcctgtagc.....ggttcacgtagtggccatc 250

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	250	100.0	2858	12 CVPT218R	X70275 pUC18 and p
2	250	100.0	2946	6 BD237489	BD237489 Genetic a
3	250	100.0	2958	12 AF327874	AF327874 Cloning v
4	250	100.0	2958	12 AF327875	AF327875 Cloning v
5	250	100.0	2958	12 ARBLKSM	X52326 pBluescript
6	250	100.0	2958	12 ARBLKSM	X52324 pBluescript
7	250	100.0	3327	6 AX138937	AX138937 Sequence
8	250	100.0	3327	6 BD000702	BD000702 Growth ho
9	250	100.0	3369	6 AX138929	AX138929 Sequence
10	250	100.0	3369	6 BD000694	BD000694 Growth ho
11	250	100.0	3379	6 AR241677	AR241677 Sequence
12	250	100.0	3394	12 AF268280	AF268280 Phagemid
13	250	100.0	3417	6 CO779544	CO779544 Sequence
14	250	100.0	3417	6 AX492865	AX492865 Sequence
15	250	100.0	3417	6 AX494199	AX494199 Sequence
16	250	100.0	3417	6 AX496673	AX496673 Sequence
17	250	100.0	3417	6 AX592730	AX592730 Sequence
18	250	100.0	3417	6 AX811486	AX811486 Sequence
19	250	100.0	3450	6 AR241678	AR241678 Sequence

C 20	250	100.0	3451	12 AF268281	AF268281 Phagemid
C 21	250	100.0	3473	6 AX766168	AX766168 Sequence
C 22	250	100.0	3473	6 AX815026	AX815026 Sequence
C 23	250	100.0	3501	6 CO779545	CO779545 Sequence
C 24	250	100.0	3501	6 AX492866	AX492866 Sequence
C 25	250	100.0	3501	6 AX494200	AX494200 Sequence
C 26	250	100.0	3501	6 AX496674	AX496674 Sequence
C 27	250	100.0	3501	6 AX592731	AX592731 Sequence
C 28	250	100.0	3501	6 AX811487	AX811487 Sequence
C 29	250	100.0	3506	12 AF416744	AF416744 Cloning v
C 30	250	100.0	3602	12 AF327894	AF327894 Cloning v
C 31	250	100.0	3621	6 AX703433	AX703433 Sequence
C 32	250	100.0	3643	12 AF327895	AF327895 Expresio
C 33	250	100.0	3656	6 166488	166488 Sequence 8
C 34	250	100.0	3688	6 166489	166489 Sequence 9
C 35	250	100.0	3732	12 AF054625	AF054625 Reporter
C 36	250	100.0	3878	6 AX105796	AX105796 Sequence
C 37	250	100.0	3954	6 AX138934	AX138934 Sequence
C 38	250	100.0	3954	6 BD000699	BD000699 Growth ho
C 39	250	100.0	3976	6 AX138930	AX138930 Sequence
C 40	250	100.0	3976	6 BD000695	BD000695 Growth ho
C 41	250	100.0	3988	6 AR300373	AR300373 Sequence
C 42	250	100.0	3988	6 AX020190	AX020190 Sequence
C 43	250	100.0	3988	6 AX079036	AX079036 Sequence
C 44	250	100.0	3988	6 BD129691	BD129691 Therapeut
C 45	250	100.0	4027	12 RVU57024	U57024 Reporter ve

ALIGNMENTS

CVPT218R 2858 bp DNA linear SYN 07-OCT-1993
pUC18 and phase f1 derivative cloning vector.
X70275 1 GI:406850
ampicillin resistance; beta-galactosidase; phase f1; pUC18 plasmid.
synthetic construct
artificial sequences.

Mead D.A., Szczesna-Skorupa E. and Kemper B.
Single-stranded DNA 'blue' T7 promoter plasmids: a versatile tandem
promoter system for cloning and protein engineering
Protein Eng. 1 (1), 67-74 (1986)
89184389
3507689

Pouwels, P.H., Enger-Valk, B.E. and Brammar, W.J.
This has no title
(in) Pouwels, P.H., Enger-Valk, B.E. and Brammar, W.J. (Eds.);
CLONING VECTORS, A LABORATORY MANUAL (SUPPL. UPDATE 1986): 1-1;
Elsevier, Amsterdam (1986)
3 (bases 1 to 2858)
Helmut Bloecker.
Direct Submission
Submitted (07-JUL-1993) Helmut Bloecker F R G,
bloecker@venus.gbf-braunschweig.d400.de
See also Pharmacia catalogue 1993/4 for description details. also:
'New pTZ18R and pTZ19R multifunctional plasmids'; Analects
13:1-2(1985).

The sequence conflicts with the vecbase 3.x entry V80071, pTZ18R as
follows: G 251 should be deleted, C 822 should be deleted, G 1095
should be A, C 2557 is followed by an additional G, A 2563 should
be deleted, bases 2839 to 2849 should be deleted, T 2862 should be
C.
#parent VecBase(3): pUC18, VecSource(3): bcgal18,
VecSource(3): Prom77, GenBank(60): f1cccg; #brother VecBase(3): pTZ19R.
Location/Qualifiers
1. .2858
/organism="synthetic construct"
/mol_type="other DNA"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 2303.51 Seconds
(without alignments)
4049.721 Million cell updates/sec

Title: US-09-747-385-15_COPY_9700_9955

Perfect score: 256

Sequence: 1 ttccgaaaagagtgtgtag.....cacatttccccgaaagtgc 256

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	190.2	74.3	971	9	CL121339 ISB1-80F2
2	185.4	72.4	266	2	AW494744 UI-M-BH3-
3	185.4	72.4	453	6	CD284564 G39169.45
4	185.4	72.4	514	6	CB878095 HP07E24T
5	185.4	72.4	514	9	CL756923 OR_BBa012
6	185.4	72.4	516	9	CL587651 OB_Ba008
7	185.4	72.4	516	9	CL618531 OR_BBa001
8	185.4	72.4	516	9	CL618532 OR_BBa001
9	185.4	72.4	516	9	CL722827 OR_BBa005
10	185.4	72.4	516	9	CL744977 OR_BBa008
11	185.4	72.4	516	9	CL744978 OR_BBa008
12	185.4	72.4	516	9	CL756924 OR_BBa012
13	185.4	72.4	517	9	CL722626 OR_BBa005
14	185.4	72.4	609	9	AG048138 Pan trogl
15	185.4	72.4	616	9	AG124170 Pan trogl
16	185.4	72.4	618	9	AG114570 Pan trogl
17	185.4	72.4	619	9	AG054036 Pan trogl
18	185.4	72.4	620	9	AG064570 Pan trogl
19	185.4	72.4	621	9	AG071608 Pan trogl
20	185.4	72.4	621	9	AG108476 Pan trogl
21	185.4	72.4	626	9	AG133646 Pan trogl
22	185.4	72.4	627	9	AG083734 Pan trogl
23	185.4	72.4	627	9	AG097424 Pan trogl
24	185.4	72.4	637	9	AG051058 Pan trogl

C 25	185.4	72.4	638	9	AG065362	Pan trogl
C 26	185.4	72.4	639	9	AG082206	Pan trogl
C 27	185.4	72.4	640	9	AG093564	Pan trogl
C 28	185.4	72.4	642	9	AG044262	Pan trogl
C 29	185.4	72.4	643	9	AG065632	Pan trogl
C 30	185.4	72.4	644	9	AG094628	Pan trogl
C 31	185.4	72.4	644	9	AG140388	Pan trogl
C 32	185.4	72.4	646	9	AG084418	Pan trogl
C 33	185.4	72.4	647	9	AG043750	Pan trogl
C 34	185.4	72.4	648	6	CB878193	HP07K15T
C 35	185.4	72.4	648	9	AG090266	Pan trogl
C 36	185.4	72.4	654	9	AG045496	Pan trogl
C 37	185.4	72.4	656	9	AG095984	Pan trogl
C 38	185.4	72.4	659	9	AG041828	Pan trogl
C 39	185.4	72.4	659	9	AG053092	Pan trogl
C 40	185.4	72.4	659	9	AG062068	Pan trogl
C 41	185.4	72.4	659	9	AG068890	Pan trogl
C 42	185.4	72.4	659	9	AG073532	Pan trogl
C 43	185.4	72.4	660	9	AG058068	Pan trogl
C 44	185.4	72.4	661	9	AG047734	Pan trogl
C 45	185.4	72.4	661	9	AG068690	Pan trogl

ALIGNMENTS

RESULT 1
CL121339
LOCUS
DEFINITION
ISB1-80F23 T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-80F23,
genomic survey sequence.
ACCESSION
CL121339
VERSION
CL121339.1 GI:40614974
KEYWORDS
GSS.
SOURCE
Xenopus tropicalis (western clawed frog)
ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE
1 (Bases 1 to 971)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
AUTHORS
A physical map of the xenopus tropicalis genome
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 75000 Std Error: 0.00
Seg primer: T7 TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence start: 15
High quality sequence stop: 604.
Location/Qualifiers
source
1. .971
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
/clones="ISB1-80F23"
/clone_lib="ISB1"
/note="Vector: pBelobAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"

ORIGIN
Query Match 74.3%; Score 190.2; DB 9; Length 971;
Best Local Similarity 93.8%; Pred. No. 1.9e-45;
Matches 198; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TTCCGAAAAGAGTGTGCTTTGATCGGCAAAACCCGCTGGTAGCGGTGGT 60
Db 91 TTCCGAAAAGAGTGTGCTTTGATCGGCAAAACCCGCTGGTAGCGGTGGT 150
Qy 61 TTTTTCCTTTTCGACGACGAGTATTCGCGCGAGAAAAAGATCTCAAGAGATCCTTTG 120

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 57.3793 Seconds
(without alignments)
3171.212 Million cell updates/sec

Title: US-09-747-385-15_COPY_9700_9955
Perfect score: 256
Sequence: 1 ttcggaaaagagttgtag.....cacatttccccgaaaagtgc 256

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	186.4	72.8	1360	3	US-09-082-649B-81
C 2	186	72.7	1360	3	US-09-082-649B-80
C 3	186	72.7	3987	3	US-09-082-649B-83
C 4	186	72.7	3987	3	US-09-082-649B-84
C 5	186	72.7	7612	4	US-09-700-934A-2
C 6	185.4	72.4	1905	1	US-08-594-469-9
C 7	185.4	72.4	1905	1	US-08-906-957-9
C 8	185.4	72.4	1947	3	US-09-025-769B-264
C 9	185.4	72.4	1947	4	US-09-490-070A-264
C 10	185.4	72.4	1947	4	US-09-490-153-264
C 11	185.4	72.4	2422	1	US-07-867-106-5
C 12	185.4	72.4	2462	4	US-09-496-445-5
C 13	185.4	72.4	2686	4	US-09-785-269C-11
C 14	185.4	72.4	2704	4	US-09-623-551-27
C 15	185.4	72.4	2755	2	US-07-916-098A-7
C 16	185.4	72.4	2839	4	US-09-809-517A-36
C 17	185.4	72.4	2865	4	US-09-795-872-9
C 18	185.4	72.4	2869	4	US-09-795-872-8
C 19	185.4	72.4	2927	2	US-08-941-647A-1
C 20	185.4	72.4	2927	3	US-09-142-481-14
C 21	185.4	72.4	2939	1	US-08-119-512-2
C 22	185.4	72.4	2939	1	US-08-488-015B-2
C 23	185.4	72.4	2939	3	US-08-814-412-17
C 24	185.4	72.4	2961	3	US-08-446-935-6
C 25	185.4	72.4	2973	4	US-09-402-266B-17
C 26	185.4	72.4	3003	6	5182260-18
C 27	185.4	72.4	3104	1	US-07-415-307A-1

28 185.4 72.4 3104 1 US-08-371-320-1 Sequence 1, Appli
29 185.4 72.4 3122 3 US-09-042-353-152 Sequence 152, App
30 185.4 72.4 3122 3 US-08-758-417A-416 Sequence 416, App
31 185.4 72.4 3130 3 US-09-038-141-1 Sequence 1, Appli
32 185.4 72.4 3138 1 US-07-867-106-4 Sequence 4, Appli
33 185.4 72.4 3175 4 US-09-646-075-2 Sequence 2, Appli
34 185.4 72.4 3175 4 US-09-027-169-6 Sequence 6, Appli
35 185.4 72.4 3190 4 US-08-507-455-4 Sequence 4, Appli
36 185.4 72.4 3249 1 US-08-737-316A-2 Sequence 2, Appli
37 185.4 72.4 3266 2 US-08-447-430A-42 Sequence 42, Appli
38 185.4 72.4 3301 2 US-09-342-673-42 Sequence 42, Appli
39 185.4 72.4 3307 3 US-09-401-171C-11 Sequence 11, Appli
40 185.4 72.4 3327 4 US-09-628-730-56 Sequence 56, Appli
41 185.4 72.4 3331 4 US-09-582-761B-32 Sequence 32, Appli
42 185.4 72.4 3343 6 5453363-2 Patent No. 5453363
43 185.4 72.4 3344 4 US-09-422-569-8 Sequence 8, Appli
44 185.4 72.4 3369 4 US-09-628-730-48 Sequence 48, Appli
45 185.4 72.4 3379 4 US-09-318-786-19 Sequence 19, Appli

ALIGNMENTS

RESULT 1

US-082-649B-81/c
; Sequence 81, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082.649B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid DNA mutant Kanamycin resistance gene
US-09-082-649B-81

Query Match 72.8%; Score 186.4; DB 3; Length 1360;
Best Local Similarity 99.5%; Pred. No. 4.1e-48;
Matches 187; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTCGAAAAAGAGTTGGTAGCTTGTATCCGCGCAACCAACCGCTGTCAGCGTGT 60
DB 1224 TTCGAAAAAGAGTTGGTAGCTTGTATCCGCGCAACCAACCGCTGTCAGCGTGT 1165
QY 61 TTTTGTTCAGACGACGATTACGGCGAGAAAAAGGATCTCAAGAGATCCTTTG 120
DB 1184 TTTTGTTCAGACGACGATTACGGCGAGAAAAAGGATCTCAAGAGATCCTTTG 1105
QY 121 ATCTTTTTCAGGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTGTC 180
DB 1104 ATCTTTTTCAGGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTGTC 1045
QY 181 ATGACGG 188
DB 1044 ATGACGTG 1037
RESULT 2

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 270.958 Seconds
(without alignments)
4959.634 Million cell updates/sec

Title: US-09-747-385-15_COPY_9700_9955

Perfect score: 256

Sequence: 1 ttccgaaaagagtggttag.....cacatttccccgaaagtgc 256

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002as: *
7: Geneseqn2002bs: *
8: Geneseqn2003as: *
9: Geneseqn2003bs: *
10: Geneseqn2003cs: *
11: Geneseqn2003ds: *
12: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256	100.0	4597	4	Aaf24901 Nucleotid
2	256	100.0	8115	6	Abag7958 Lactic ac
3	256	100.0	8115	6	Abag7959 Lactic ac
4	189.8	74.1	5195	6	Abq74554 Human Del
5	189.8	74.1	5195	12	Adm94827 Human dev
6	189.8	74.1	5566	6	Abn86160 Nucleotid
c 7	187.2	73.1	3851	12	Adp80954 Vector pD
c 8	187	73.0	1824	4	Aas41089 cDNA enco
c 9	187	73.0	1824	4	Aak57143 Human imm
10	186.8	73.0	6756	12	Adj57431 Vector pA
11	186.8	73.0	6757	6	Aas20498 Expressio
12	186.6	72.9	5875	8	Abz75111 VEGF expr
13	186.4	72.8	5742	6	Aas20504 Expressio
14	186.4	72.8	5742	12	Adj57437 Vector pY
15	186.4	72.8	10160	12	Adp84798 HIV subty
16	186.4	72.8	10186	12	Adp84796 Plasmid c
17	186.4	72.8	10198	12	Adp84799 HIV subty
18	186.2	72.7	5091	10	Adi39129 B. subtil
19	186.2	72.7	5091	12	Ado80519 Plasmid p
20	186.2	72.7	5091	12	Ado80585 Plasmid p
21	186.2	72.7	5091	12	Ado80330 Plasmid p

22	186.2	72.7	5156	10	ADP66614
23	186.2	72.7	5156	12	ADQ31509
24	186.2	72.7	6087	10	ADP66615
25	186.2	72.7	6087	12	ADQ31510
26	186.2	72.7	8787	10	ADI39145
c 27	186	72.7	1360	2	AAV74262
c 28	186	72.7	1360	2	AAV83728
c 29	186	72.7	3647	12	ADL90416
30	186	72.7	4204	3	AAC55522
31	186	72.7	4208	3	AAC55523
c 32	186	72.7	4470	3	AAC55521
c 33	186	72.7	4470	10	ABZ58767
c 34	186	72.7	4886	12	ADL90418
c 35	186	72.7	4892	9	ADA50329
c 36	186	72.7	5076	12	ADL90417
37	186	72.7	5584	3	AAC55632
38	186	72.7	5584	10	ABZ58766
39	186	72.7	7612	3	AAZ39629
40	185.6	72.5	9830	3	AAA96220
41	185.6	72.5	10704	2	AAQ43846
c 42	185.4	72.4	478	8	AAAD48705
c 43	185.4	72.4	478	10	ADC13870
c 44	185.4	72.4	695	2	AAV69310
c 45	185.4	72.4	941	12	ADO36316

ALIGNMENTS

RESULT 1
AAF24901
ID AAF24901 standard; DNA; 4597 BP.
XX
AC AAF24901;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of the plasmid pCDNA3.1/GS.

XX
KW Microsphere; dihydrazide; hyaluronic acid; inflammatory response;
KW myocardial ischemia; cardiac angiogenesis; haemophilia;
KW vascular endothelial growth factor; VEGF; ss.

OS Synthetic.

XX
FN WO200078358-A2.

XX
PD 28-DEC-2000.

XX
PF 19-JUN-2000; 2000WO-US016837.

XX
PR 18-JUN-1999; 99US-0140260P.

(COLL-) COLLABORATIVE GROUP LTD.

Chen W;

DR WPI; 2001-071363/08.

XX
PT Hyaluronic acid micro spheres for use in gene therapy of myocardial
PT ischemia and hemophilla, comprising dihydrazide derivatized hyaluronic
PT acids crosslinked to nucleic acids.

XX
PS Example 1; Page 36-38; 38pp; English.

XX
CC The specification describes a microsphere comprising dihydrazide
CC derivatised hyaluronic acid crosslinked to a nucleic acid (NA). The
CC microspheres cause reduced inflammatory responses, and have increased
CC safety and biodegradability. The microspheres are useful for transfecting
CC a cell of a subject and for treating a subject having myocardial
CC ischemia, by increasing cardiac angiogenesis. They are also useful for
CC treating haemophilia. The present sequence represents the plasmid
CC pCDNA3.1/GS, into which is inserted a polynucleotide sequence which is

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 10:02:48 ; Search time 1243.71 Seconds
(without alignments)
9733.921 Million cell updates/sec

Title: US-09-747-385-15_COPY_9700_9955
Perfect score: 256
Sequence: 1 ttccgaaaaagattgtagtgc.....cacatttccccgaaaaagtgc 256

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	256	100.0	3986	12 PCDNA3ZEO	X90639 Cloning vec
2	256	100.0	4392	12 AF361441	AF361441 Cloning v
3	256	100.0	4597	6 AX060344	AX060344 Sequence
4	256	100.0	8115	6 BD087749	BD087749 Shuttle v
5	256	100.0	8115	6 BD087750	BD087750 Shuttle v
6	190	74.2	4419	12 AY219688	AY219688 Expressio
7	189.8	74.1	5566	6 AX451644	AX451644 Sequence
8	188.8	73.8	6023	12 AF102577	AF102577 Cloning v
9	187	73.0	4952	12 XXU14594	U14594 Shuttle vec
10	187	73.0	131002	2 AC024392	AC024392 Homo sapi
11	186.8	73.0	6757	6 CQ760746	CQ760746 Sequence
12	186.8	73.0	6757	6 AX451313	AX451313 Sequence
13	186.6	72.9	5874	6 AX615156	AX615156 Sequence
14	186.6	72.9	5875	6 AX754988	AX754988 Sequence
15	186.4	72.8	1360	6 AR182909	AR182909 Sequence
16	186.4	72.8	4050	12 AF053407	AF053407 Expressio
17	186.4	72.8	4227	12 AF053408	AF053408 Expressio
18	186.4	72.8	4625	12 AF053409	AF053409 Expressio
19	186.4	72.8	5742	6 CQ760752	CQ760752 Sequence

20	186.4	72.8	5742	6	AX451319	Sequence
21	186.2	72.7	5091	6	CQ794458	Sequence
22	186.2	72.7	5091	6	CQ794562	Sequence
23	186.2	72.7	5091	6	CQ795592	Sequence
24	186.2	72.7	5091	6	AX930591	Sequence
25	186.2	72.7	5091	6	AX959595	Sequence
26	186.2	72.7	5156	6	CQ826646	Sequence
27	186.2	72.7	6087	6	CQ826647	Sequence
28	186.2	72.7	6142	6	CQ795604	Sequence
29	186.2	72.7	6472	6	CQ794470	Sequence
30	186.2	72.7	6591	6	CQ794576	Sequence
31	186.2	72.7	6631	6	AX959601	Sequence
32	186.2	72.7	6631	6	AX959605	Sequence
33	186.2	72.7	8384	12	AX265466	Shuttle v
34	186.2	72.7	8787	6	AX930607	Sequence
35	186	72.7	1360	6	AR182908	Sequence
36	186	72.7	2730	12	AY219701	AY219701 Cloning v
37	186	72.7	3018	12	AF324725	AF324725 Cloning v
38	186	72.7	3090	12	AF223640	AF223640 Cloning v
39	186	72.7	3141	12	AF324726	AF324726 Cloning v
40	186	72.7	3647	6	CQ794766	Sequence
41	186	72.7	3987	6	AR182910	Sequence
42	186	72.7	3987	6	AR182911	Sequence
43	186	72.7	4204	6	BD263378	Compositi
44	186	72.7	4208	6	BD263379	Compositi
45	186	72.7	4470	6	BD263377	Compositi

ALIGNMENTS

RESULT 1
PCDNA3ZEO Cloning vector pcdna32eo DNA. 3986 bp DNA linear SYN 16-AUG-1995
X90639.1 GI:949972
cloning vector; expression vector; multiple cloning site; Plasmid.
synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
Peters,H., Hundhausen,T., Kroenke,M. and Marget,M.
TITLE A new small sized high-level eukaryotic expression vector
JOURNAL Unpublished
AUTHORS Peters,H.
TITLE Direct Submission
JOURNAL Submitted (07-AUG-1995) H. Peters, Inst. f. Immunologie,
Michaelisstr.5, D- 24105 Kiel, FRG
COMMENT Related sequences: M21295 and K03104.
FEATURES Location/Qualifiers
source 1..3986
/organism="synthetic construct"
/mol_type="other DNA"
/db_xref="taxon:32630"
/plasmid="pcDNA32EO"
misc_feature 1..2125
/note="cloning vector (pcDNA3) (Invitrogen)"
misc_feature 889..994
/note="multiple cloning site (MCS)"
misc_feature 2126..2796
/note="Cloning vector (PzeoSV) (Invitrogen)"
misc_feature 2797..3986
/note="cloning vector (pcDNA3)"

ORIGIN
Query Match 100.0%; Score 256; DB 12; Length 3986;
Best Local Similarity 100.0%; Pred. No. 8.4e-65;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAAAAAGATTGGTAGCTTGTATCCGCAACAAACACCGCTGGTAGCGTGGT 60
|||||

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OM nucleic - nucleic search, using sw model

Run on: January 5, 2005, 12:44:02 ; Search time 1168.43 Seconds
(without alignments)
1237.519 Million cell updates/sec

Title: US-09-747-385-15_COPY_9700_9955

Perfect score: 256

Sequence: 1 ttccgaaaagtggttag.....cacattcccgaaaagtgc 256

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	256	100.0	4597	15	US-10-277-184-3
2	256	100.0	8115	9	US-09-778-516A-1
3	256	100.0	8115	9	US-09-778-516A-2
4	189.8	74.1	5195	16	US-10-419-045-2
5	189.8	74.1	5566	15	US-10-400-053-22
6	186.8	73.0	6757	9	US-09-896-594-16
7	186.8	73.0	6757	16	US-10-185-475-16
8	186.8	73.0	6757	16	US-10-672-484-16
c 9	186.4	72.8	1360	11	US-09-965-101-81
10	186.4	72.8	5742	9	US-09-896-594-22
11	186.4	72.8	5742	16	US-10-185-475-22
12	186.4	72.8	5742	16	US-10-672-484-22

13	186.2	72.7	5156	15	US-10-307-138-12	Sequence 12, Appl
14	186.2	72.7	6087	15	US-10-307-138-13	Sequence 13, Appl
c 15	186	72.7	1360	11	US-09-965-101-80	Sequence 80, Appl
16	186	72.7	3647	15	US-10-241-596-134	Sequence 134, Appl
c 17	186	72.7	3715	17	US-10-446-629-5	Sequence 5, Appl
c 18	186	72.7	3741	17	US-10-446-629-4	Sequence 4, Appl
19	186	72.7	3987	11	US-09-965-101-83	Sequence 83, Appl
c 20	186	72.7	3987	11	US-09-965-101-84	Sequence 21, Appl
c 21	186	72.7	4470	15	US-10-151-690-21	Sequence 136, Appl
c 22	186	72.7	4886	15	US-10-241-596-136	Sequence 1, Appl
c 23	186	72.7	4892	15	US-10-357-268-1	Sequence 135, Appl
c 24	186	72.7	5076	15	US-10-241-596-135	Sequence 61, Appl
c 25	186	72.7	5584	15	US-10-151-690-61	Sequence 115, Appl
c 26	185.4	72.4	478	15	US-10-260-150-115	Sequence 267259,
27	185.4	72.4	641	13	US-10-027-632-267259	Sequence 267259,
28	185.4	72.4	641	15	US-10-027-632-267259	Sequence 1385, Ap
c 29	185.4	72.4	1150	9	US-09-764-868-1385	Sequence 1380, Ap
c 30	185.4	72.4	1796	9	US-09-764-868-1380	Sequence 8685, Ap
c 31	185.4	72.4	1796	10	US-09-764-891-8685	Sequence 6091, Ap
c 32	185.4	72.4	1953	9	US-09-974-300-6091	Sequence 5564, Ap
c 33	185.4	72.4	2210	10	US-09-764-891-5564	Sequence 5568, Ap
c 34	185.4	72.4	2212	10	US-09-764-891-5568	Sequence 5577, Ap
c 35	185.4	72.4	2212	10	US-09-764-891-5577	Sequence 5579, Ap
c 36	185.4	72.4	2212	10	US-09-764-891-5579	Sequence 5599, Ap
c 37	185.4	72.4	2212	10	US-09-764-891-5599	Sequence 5607, Ap
c 38	185.4	72.4	2212	10	US-09-764-891-5607	Sequence 5609, Ap
c 39	185.4	72.4	2212	10	US-09-764-891-5609	Sequence 5572, Ap
c 40	185.4	72.4	2213	10	US-09-764-891-5572	Sequence 5502, Ap
c 41	185.4	72.4	2213	10	US-09-764-891-5602	Sequence 11, Appl
c 42	185.4	72.4	2297	10	US-09-891-865A-11	Sequence 14, Appl
43	185.4	72.4	2406	15	US-10-307-138-14	Sequence 5, Appl
44	185.4	72.4	2462	15	US-10-365-062-5	Sequence 1, Appl
45	185.4	72.4	2570	9	US-09-836-737A-1	

ALIGNMENTS

RESULT 1

US-10-277-184-3
; Sequence 3, Application US/10277184
; Publication No. US20030114406A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Weiliam
; TITLE OF INVENTION: HYALURONIC ACID MICROSPHERES FOR
; FILE REFERENCE: 2055/1G717-US1
; CURRENT APPLICATION NUMBER: US/10/277,184
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/596,665
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 60/140,260
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4597
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pCDNA3.1/GS vector by Invitrogen Corporation
US-10-277-184-3

Query Match	100.0%	Score 256;	DB 15;	Length 4597;
Best Local Similarity	100.0%	Pred. No. 6.6e-69;	Indels 0;	Gaps 0;
Matches 256;	Conservative 0;	Mismatches 0;		
Qy	1	TTCCGAAAAGAGTGGTAGCTTTGATCCGGCAAAACACCGCTGGTAGCGGTGGT 60		
Db	4331	TTCCGAAAAGAGTGGTAGCTTTGATCCGGCAAAACACCGCTGGTAGCGGTGGT 4390		
Qy	61	TTTTTTGTTTCAGACGACGATACGGCGCAAAAAGGATCTCAAGAGATCCTTTG 120		